

AMENDMENTS TO THE CLAIMS, COMPLETE LISTING OF CLAIMS
IN ASCENDING ORDER WITH STATUS INDICATOR

Please amend the following claims as indicated.

1. (Currently Amended) A metal complex ~~which has comprising~~ a functional group ~~capable of forming~~ which is to form a covalent bond with an amino group of an N-terminal amino acid residue of protein or peptide or with a carboxyl group of a C-terminal amino acid residue of protein or peptide, ~~wherein the covalent bond to be formed between the amino group of the N-terminal amino acid residue of protein or peptide or the carboxyl group of the C-terminal amino acid residue of protein or peptide and the functional group is not cleaved in a stage of ionization in mass spectrometry.~~

2. (Currently Amended) The metal complex according to claim 1, ~~which has further comprising a ligand with the said~~ functional group ~~capable of forming~~ which is to form the covalent bond with the amino group of the N-terminal amino acid residue of protein or peptide or with the carboxyl group of the C-terminal amino acid residue of protein or peptide.

3. (Original) The metal complex according to claim 1, wherein a metal element thereof is selected from transition metals and typical metals.

4. (Original) The metal complex according to claim 1, wherein a coordination number thereof is 2, 3, 4, 5 or 6.

5. (Original) The metal complex according to claim 1, wherein a ligand thereof is a monodentate ligand or a polydentate ligand.

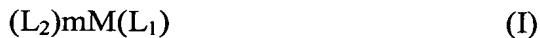
6. (Canceled).

7. (Currently Amended) The metal complex according to claim 1, wherein the functional group ~~capable of forming~~ which is to form the covalent bond with the amino group of

the N-terminal amino acid residue of protein or peptide is a functional group capable of forming which is to form the covalent bond through nucleophilic reaction with the amino group.

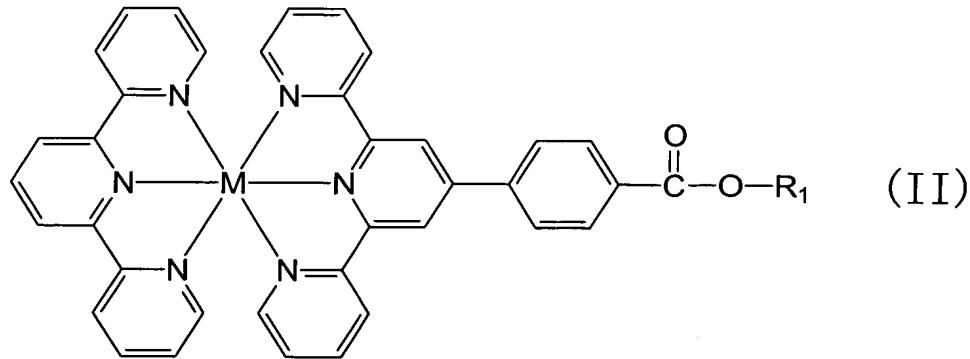
8. (Currently Amended) The metal complex according to claim 1, wherein the functional group capable of forming which is to form the covalent bond with the amino group of the N-terminal amino acid residue of protein or peptide is -CO-OR₁, where R₁ represents H or an active ester-forming group.

9. (Original) The metal complex according to claim 1, which is represented by the following general formula (I):

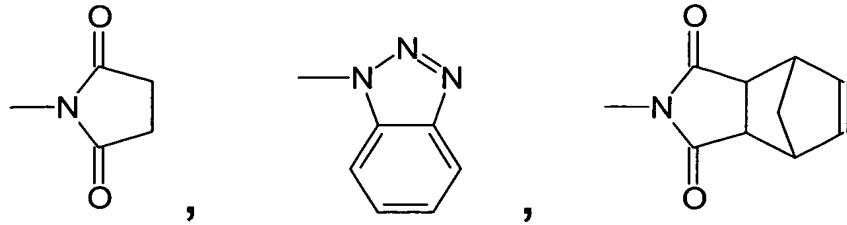


wherein M represents a transition metal; L₁ represents a ligand having a substituent: -CO-OR₁ (where R₁ represents H or an active ester-forming group) or -R₂-CO-OR₁ (where R₂ represents an arylene group or an alkylene group, R₁ represents H or an active ester-forming group); L₂ represents a ligand; m is a number of L₂, indicating 0, 1, 2, 3, 4 or 5.

10. (Original) The metal complex according to claim 1, which is represented by the following general formula (II):



wherein M represents a transition metal; and R₁ represents H or an active ester-forming group represented by any of the following formula:



11. (Currently Amended) The metal complex according to claim 1, wherein the functional group ~~capable of forming which is to form~~ the covalent bond with the carboxyl group of the C-terminal amino acid residue of protein or peptide is a functional group ~~capable of forming which is to form~~ the covalent bond through nucleophilic reaction with the carboxyl group.

12. (Currently Amended) The metal complex according to 1, wherein the functional group ~~capable of forming which is to form~~ the covalent bond with the carboxyl group of the C-terminal amino acid residue of protein or peptide is -NH₂ or -NHNH₂.

13. (Original) The metal complex as claimed in claim 1, which is represented by the following general formula (III):



wherein M represents a transition metal; L₃ represents a ligand having a substituent: -NH₂, -NHNH₂, -R₂-NH₂ or -R₂-NHNH₂ (where R₂ represents an arylene group or an alkylene group); L₂ represents a ligand; m is a number of L₂, indicating 0, 1, 2, 3, 4 or 5.

14. (Original) A reagent for determining amino acid sequence of protein or peptide, which comprises the metal complex according to claim 1.

15. (Original) A method for determining amino acid sequence of protein or peptide, which comprises using the metal complex according to claim 1.

16. (Original) A method for determining amino acid sequence of protein or peptide, which comprises

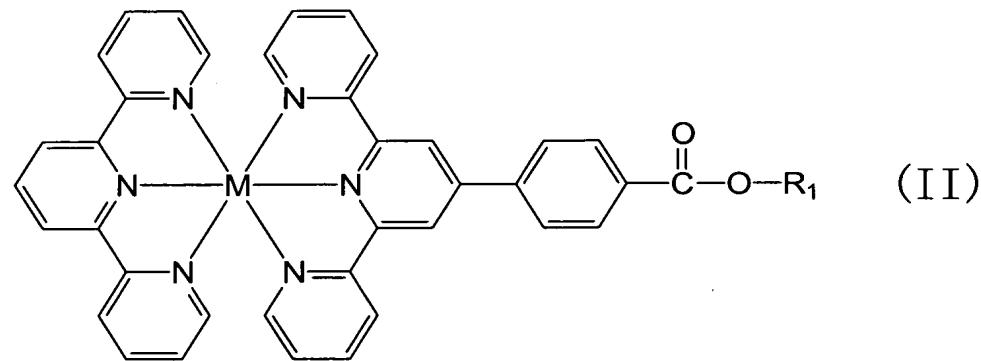
reacting the metal complex according to claim 1 with a protein or peptide (A) of which the amino acid sequence is to be determined, to form a metal complex derivative (B) where the covalent bond of the functional group of the metal complex with the amino group of the N-terminal amino acid residue of the protein or peptide (A) or with the carboxyl group of the C-terminal amino acid residue of protein or peptide is formed, and
analyzing the metal complex derivative (B) through mass spectrometry.

17. (New) A metal complex comprising a functional group which is to form a covalent bond with an amino group of an N-terminal amino acid residue of protein or peptide, wherein the metal complex is represented by the following general formula (I):

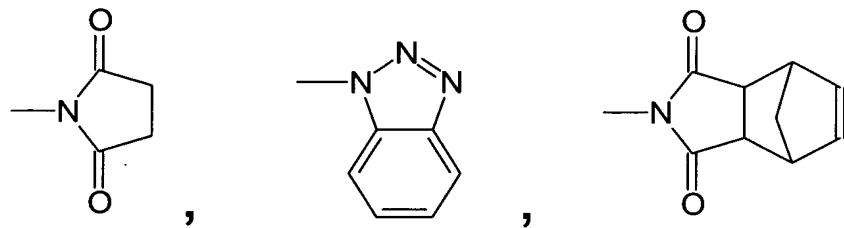


wherein M represents a transition metal; L₁ represents a ligand having a substituent: -CO-OR₁ (where R₁ represents H or an active ester-forming group) or -R₂-CO-OR₁ (where R₂ represents an arylene group, R₁ represents H or an active ester-forming group); L₂ represents a ligand; m is a number of L₂, indicating 0, 1, 2, 3, 4 or 5.

18. (New) The metal complex according to claim 17, which is represented by the following general formula (II):



wherein M represents a transition metal; and R₁ represents H or an active ester-forming group represented by any of the following formula:



19. (New) A metal complex comprising a functional group which is to form a covalent bond with a carboxyl group of a C-terminal amino acid residue of protein or peptide, wherein the functional group which is to form the covalent bond with the carboxyl group of the C-terminal amino acid residue of protein or peptide is -NHNH₂.

20. (New) The metal complex according to claim 19, which is represented by the following general formula (III):



wherein M represents a transition metal; L₃ represents a ligand having a substituent: -NHNH₂ or -R₂-NHNH₂ (where R₂ represents an arylene group or an alkylene group); L₂ represents a ligand; m is a number of L₂, indicating 0, 1, 2, 3, 4 or 5.

21. (New) A method for determining amino acid sequence of protein or peptide, which comprises

reacting a metal complex which comprises a functional group which is to form a covalent bond with an amino group of an N-terminal amino acid residue of protein or peptide or with a carboxyl group of a C-terminal amino acid residue of protein or peptide, with a protein or peptide (A) of which the amino acid sequence is to be determined, to form a metal complex derivative (B) where the covalent bond of the functional group of the metal complex with the amino group of the N-terminal amino acid residue of the protein or peptide (A) or with the carboxyl group of the C-terminal amino acid residue of protein or peptide is formed, and analyzing the metal complex derivative (B) through mass spectrometry.